

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Bendele, Alison M.
Sennello, Regina M.
Edwards, Carl K.

(ii) TITLE OF INVENTION: COMBINATION THERAPY USING A TNF BINDING
PROTEIN FOR TREATING TNF-MEDIATED DISEASES

(iii) NUMBER OF SEQUENCES: 4

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Amgen Inc.
(B) STREET: 1840 DeHavilland Drive
(C) CITY: Thousand Oaks
(D) STATE: CA
(E) COUNTRY: US
(F) ZIP: 91320-1789

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: NOT YET KNOWN
(B) FILING DATE: 08-DEC-1997
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/032,587
(B) FILING DATE: 06-DEC-1996

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/036,355
(B) FILING DATE: 23-JAN-1997

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/039,315
(B) FILING DATE: 07-FEB-1997

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/052,023
(B) FILING DATE: 09-JUL-1997

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Zindrick, Thomas K.
(B) REGISTRATION NUMBER: 32,185
(C) REFERENCE/DOCKET NUMBER: A-430D

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 483 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

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(ix) FEATURE:
      (A) NAME/KEY: CDS
      (B) LOCATION: 1..483
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GAT Asp 1	AGT Ser	GTG Val	TGT Cys	CCC Pro 5	CAA Gln	GGA Gly	AAA Lys	TAT Tyr	ATC Ile 10	CAC His	CCT Pro	CAA Gln	AAT Asn 15	AAT Asn	TCG Ser	48
ATT Ile	TGC Cys	TGT Cys	ACC Thr 20	AAG Lys	TGC Cys	CAC His	AAA Lys	GGA Gly 25	ACC Thr	TAC Tyr	TTG Leu	TAC Tyr	AAT Asn 30	GAC Asp	TGT Cys	96
CCA Pro	GGC Gly 35	CCG Pro	GGG Gly	CAG Gln	GAT Asp	ACG Thr	GAC Asp 40	TGC Cys	AGG Arg	GAG Glu	TGT Cys 45	GAG Glu	AGC Ser	GGC Gly	TCC Ser	144
TTC Phe 50	ACC Thr	GCT Ala	TCA Ser	GAA Glu	AAC Asn	CAC His 55	CTC Leu	AGA Arg	CAC His	TGC Cys	CTC Leu 60	AGC Ser	TGC Cys	TCC Ser	AAA Lys	192
TGC Cys 65	CGA Arg	AAG Lys	GAA Glu	ATG Met 70	GGT Gly	CAG Gln	GTG Val 75	GAG Glu	ATC Ile	TCT Ser 75	TCT Ser	TGC Cys	ACA Thr	GTG Val	GAC Asp 80	240
CGG Arg	GAC Asp	ACC Thr	GTG Val	TGT Cys 85	GGC Gly	TGC Cys	AGG Arg	AAG Lys	AAC Asn 90	CAG Gln	TAC Tyr	CGG Arg	CAT His	TAT Tyr 95	TGG Trp	288
AGT Ser	GAA Glu	AAC Asn 100	CTT Leu	TTC Phe	CAG Gln	TGC Cys	TTC Phe 105	AAT Asn	TGC Cys	AGC Ser	CTC Leu	TGC Cys 110	CTC Leu	AAT Asn	GGG Gly	336
ACC Thr	GTG Val 115	CAC His	CTC Leu	TCC Ser	TGC Cys	CAG Gln	GAG Glu 120	AAA Lys	CAG Gln	AAC Asn	ACC Thr	GTG Val 125	TGC Cys	ACC Thr	TGC Cys	384
CAT His 130	GCA Ala	GGT Gly	TTC Phe	TTT Phe	CTA Leu	AGA Arg 135	GAA Glu	AAC Asn 140	GAG Glu	TGT Cys	GTC Val	TCC Ser	TGT Cys	AGT Ser	AAC Asn	432

480

483

(i) SEQUENCE CHARACTERISTICS:

- SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 161 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

[illegible]

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 705 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..705

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TTG CCC GCC CAG GTG GCA TTT ACA CCC TAC GCC CCG GAG CCC GGG AGC	48
Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser	
1 5 10 15	
ACA TGC CGG CTC AGA GAA TAC TAT GAC CAG ACA GCT CAG ATG TGC TGC	96
Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys	
20 25 30	
AGC AAG TGC TCG CCG GGC CAA CAT GCA AAA GTC TTC TGT ACC AAG ACC	144
Ser Lys Cys Ser Pro Gly Gln His Ala Lys Val Phe Cys Thr Lys Thr	
35 40 45	
TCG GAC ACC GTG TGT GAC TCC TGT GAG GAC AGC ACA TAC ACC CAG CTC	192
Ser Asp Thr Val Cys Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu	
50 55 60	
TGG AAC TGG GTT CCC GAG TGC TTG AGC TGT GGC TCC CGC TGT AGC TCT	240
Trp Asn Trp Val Pro Glu Cys Leu Ser Cys Gly Ser Arg Cys Ser Ser	
65 70 75 80	
GAC CAG GTG GAA ACT CAA GCC TGC ACT CGG GAA CAG AAC CGC ATC TGC	288
Asp Gln Val Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn Arg Ile Cys	
85 90 95	
ACC TGC AGG CCC GGC TGG TAC TGC GCG CTG AGC AAG CAG GAG GGG TGC	336
Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln Glu Gly Cys	
100 105 110	
CGG CTG TGC GCG CCG CTG CGC AAG TGC CGC CCG GGC TTC GGC GTG GCC	384
Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly Val Ala	
115 120 125	
AGA CCA GGA ACT GAA ACA TCA GAC GTG GTG TGC AAG CCC TGT GCC CCG	432
Arg Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala Pro	
130 135 140	
GGG ACG TTC TCC AAC ACG ACT TCA TCC ACG GAT ATT TGC AGG CCC CAC	480
Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr Asp Ile Cys Arg Pro His	
145 150 155 160	

CAG ATC TGT AAC GTG GTG GCC ATC CCT GGG AAT GCA AGC AGG GAT GCA	528
Gln Ile Cys Asn Val Val Ala Ile Pro Gly Asn Ala Ser Arg Asp Ala	
165 170 175	
GTC TGC ACG TCC ACG TCC CCC ACC CGG AGT ATG GCC CCA GGG GCA GTA	576
Val Cys Thr Ser Thr Ser Pro Thr Arg Ser Met Ala Pro Gly Ala Val	
180 185 190	
CAC TTA CCC CAG CCA GTG TCC ACA CGA TCC CAA CAC ACG CAG CCA ACT	624
His Leu Pro Gln Pro Val Ser Thr Arg Ser Gln His Thr Gln Pro Thr	
195 200 205	
CCA GAA CCC AGC ACT GCT CCA AGC ACC TCC TTC CTG CTC CCA ATG GGC	672
Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser Phe Leu Leu Pro Met Gly	
210 215 220	
CCC AGC CCC CCA GCT GAA GGG AGC ACT GGC GAC	705
Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly Asp	
225 230 235	

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser	
1 5 10 15	
Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys	
20 25 30	
Ser Lys Cys Ser Pro Gly Gln His Ala Lys Val Phe Cys Thr Lys Thr	
35 40 45	
Ser Asp Thr Val Cys Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu	
50 55 60	
Trp Asn Trp Val Pro Glu Cys Leu Ser Cys Gly Ser Arg Cys Ser Ser	
65 70 75 80	
Asp Gln Val Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn Arg Ile Cys	
85 90 95	
Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln Glu Gly Cys	
100 105 110	
Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly Val Ala	
115 120 125	

Arg Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala Pro
130 135 140

Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr Asp Ile Cys Arg Pro His
145 150 155 160

Gln Ile Cys Asn Val Val Ala Ile Pro Gly Asn Ala Ser Arg Asp Ala
165 170 175

Val Cys Thr Ser Thr Ser Pro Thr Arg Ser Met Ala Pro Gly Ala Val
180 185 190

His Leu Pro Gln Pro Val Ser Thr Arg Ser Gln His Thr Gln Pro Thr
195 200 205

Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser Phe Leu Leu Pro Met Gly
210 215 220

Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly Asp
225 230 235